

SEQUENCE LISTING

<110> Brugliera, Filippa  
Holton, Timothy A.  
Michael, Michael Z.

<120> GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES  
AND USES THEREFOR

<130> 11658

<140> 09/142,108  
<141> 1998-09-01

<150> PN8386  
<151> 1996-03-01

<160> 45

<170> PatentIn Ver. 2.1

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Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro.  
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ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202  
Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro  
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Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu  
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Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp			
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cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat			442
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Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His			
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Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala			
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Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr			
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Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly			
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Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val			
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caa ctt aat tgg tta gat att caa ggt gta gcc gct aaa atg aag aag			778
Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys Lys			
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Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu His			
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Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu Ile			
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Thr Glu Ile Lys Ala Leu Leu Asn Leu Phe Val Ala Gly Thr Asp			
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Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val Gly			
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Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr Leu			
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gaa gct ata gtc aag gaa acc ttt cgg ctt cat cca tca acc cct ctt			1162
Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu			
360	365	370	
tca ctt cct aga att gca tct gag agt tgt gag atc aat ggc tat ttc			1210
Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr Phe			
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Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala Ile Ala Arg			
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Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe			
405	410	415	
ttg cca gga ggt gag aag ccc aaa gtt gat gtc cgt ggg aat gac ttt			1354
Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp Phe			
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gaa gtc ata cca ttt gga gct gga cgt agg att tgt gct gga atg aat			1402
Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Asn			
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Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His Ala			
455	460	465	
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Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn Met			
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Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro Leu Val Val			
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His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly			
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agtttggta tgcttggat ttagtagtt ttatattgat agatcaatgt ttgcattgtc	1708		
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Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr  
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Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala  
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Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn  
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Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn  
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Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu  
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Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp  
130 135 140  
Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu  
145 150 155 160  
Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val  
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Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe  
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Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp  
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Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser  
260 265 270  
Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys  
275 280 285  
Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala  
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Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu  
305 310 315 320  
Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys  
325 330 335  
Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu  
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Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser  
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 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala  
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 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly  
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 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala  
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 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu  
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 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met  
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 aaaaaaaaaatt ataatgtcac ccttagaggt aactttctac accatagtcc t atg cac 177  
 Met His  
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 aat ctc tac tac ctc atc acc acc gtc ttc cgc ggc cac caa aaa ccg 225  
 Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro  
 5 10 15  
  
 ctt cct cca ggg cca cga cca tgg ccc atc gtg gga aac ctc cca cat 273  
 Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His  
 20 25 30  
  
 atg ggc cag gca ccg cac cag ggc tta gca gcc ctg gcg caa aag tat 321  
 Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr  
 35 40 45 50  
  
 ggc cct cta ttg tat atg aga ctg ggg tac gtg gac gtt gtt gtg gcc 369  
 Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val Ala  
 55 60 65  
  
 gcc tca gcg tct gta gcg acc cag ttt ctt aag aca cat gac cta aat 417

Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp Leu Asn	70	75	80		
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tat caa gac ctt gtt ttt gca cct tat gga cct aaa tgg cgc atg ctt Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu	100	105	110	513	
agg aaa att tgt tcc tta cac atg ttt tct tct aag gct ttg gac gat Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp	115	120	125	130	561
ttt aga ctt gtc cgt cag gaa gaa gta tct ata ctg gta aat gcg ata Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn Ala Ile	135	140	145	609	
gca aaa gca gga aca aag cca gta caa cta gga caa cta ctc aac gtg				657	
Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu Asn Val	150	155	160		
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ggt gat ggc aca ggg aaa agc gac cca aaa gcc gag gaa ttt aag gac				753	
Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Asp	180	185	190		
atg gtg ctg gag tta atg gtt ctc acc gga gtt ttt aac att ggc gat Met Val Leu Glu Leu Met Val Leu Thr Gly Val Phe Asn Ile Gly Asp	195	200	205	210	801
ttt gta ccg gca ttg gaa tgt cta gac tta caa ggt gtt gca tct aaa Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala Ser Lys	215	220	225	849	
atg aag aaa tta cat aaa aga ctt gat aat ttt atg agt aac att ttg Met Lys Lys Leu His Lys Arg Leu Asp Asn Phe Met Ser Asn Ile Leu	230	235	240	897	
gag gaa cac aag agt gtt gca cat caa caa aat ggt gga gat ttg cta Glu Glu His Lys Ser Val Ala His Gln Gln Asn Gly Gly Asp Leu Leu	245	250	255	945	
agc att ttg ata tct ttg aag gat aat tgt gat ggt gaa ggt ggc aag Ser Ile Leu Ile Ser Leu Lys Asp Asn Cys Asp Gly Glu Gly Gly Lys	260	265	270	993	
ttt agt gcc aca gaa att aag gcc ttg cta ttg gat tta ttt aca gct Phe Ser Ala Thr Glu Ile Lys Ala Leu Leu Asp Leu Phe Thr Ala	275	280	285	290	1041
gga aca gac aca tca tct agt aca act gaa tgg gcc ata gcc gaa cta				1089	

Gly Thr Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala Glu Leu	295	300	305	
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gtc gtg ggc cga gac cga ctc ata gcc gaa gct gac ata ccg aac cta Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro Asn Leu	325	330	335	1185
acc tac ttc caa gcc gta atc aaa gag gtt ttc cga ctt cac ccg tcc Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His Pro Ser	340	345	350	1233
acc ccg ctt tcc cta cca cgg gtc gca aac gaa tcg tgc gaa ata aac Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu Ile Asn	355	360	365	1281
ggg tac cac att ccc aaa aac acc act tta ttg gta aat gtg tgg gcc Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val Trp Ala	375	380	385	1329
atc gca cgc gac cct gag gtt tgg gcc gac ccg tta gag ttt aaa ccc Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe Lys Pro	390	395	400	1377
gaa aga ttt ttg ccg ggc ggc gaa aag ccc aat gtg gat gtg aaa gga Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly	405	410	415	1425
aac gat ttt gag ctg att ccg ttc ggg gcg ggc cga cgg att tgt gct Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala	420	425	430	1473
ggg ctg agt ttg ggc ctg cgt atg gtc cag ttg atg aca gcc act ttg Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala Thr Leu	435	440	445	1521
gcc cat act tat gat tgg gcc tta gct gat ggg ctt atg ccc gaa aag Ala His Thr Tyr Asp Trp Ala Leu Ala Asp Gly Leu Met Pro Glu Lys	455	460	465	1569
ctt aac atg gat gag gct tat ggg ctt acc tta cag cgt aag gtg cca Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys Val Pro	470	475	480	1617
ctt aat ggt cca ccc gac ccc gtc ggc ttc tcg gcc cgt gtt taa Leu Asn Gly Pro Pro Asp Pro Val Gly Phe Ser Ala Arg Val	485	490	495	1662
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<213> Dianthus caryophyllus

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Pro His Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln  
35 40 45  
Lys Tyr Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val  
50 55 60  
Val Ala Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp  
65 70 75 80  
Leu Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala  
85 90 95  
Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg  
100 105 110  
Met Leu Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu  
115 120 125  
Asp Asp Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn  
130 135 140  
Ala Ile Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu  
145 150 155 160  
Asn Val Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg  
165 170 175  
Val Leu Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe  
180 185 190  
Lys Asp Met Val Leu Glu Leu Met Val Leu Thr Gly Val Phe Asn Ile  
195 200 205  
Gly Asp Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala  
210 215 220  
Ser Lys Met Lys Lys Leu His Lys Arg Leu Asp Asn Phe Met Ser Asn  
225 230 235 240  
Ile Leu Glu Glu His Lys Ser Val Ala His Gln Gln Asn Gly Gly Asp  
245 250 255  
Leu Leu Ser Ile Leu Ile Ser Leu Lys Asp Asn Cys Asp Gly Glu Gly  
260 265 270  
Gly Lys Phe Ser Ala Thr Glu Ile Lys Ala Leu Leu Leu Asp Leu Phe  
275 280 285  
Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Thr Glu Trp Ala Ile Ala  
290 295 300  
Glu Leu Ile Arg His Pro Lys Ile Leu Ala Gln Val Gln Glu Met  
305 310 315 320  
Asp Ser Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro  
325 330 335  
Asn Leu Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His  
340 345 350  
Pro Ser Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu  
355 360 365  
Ile Asn Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val  
370 375 380  
Trp Ala Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe  
385 390 395 400  
Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val  
405 410 415  
Lys Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile

420	425	430
Cys Ala Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala		
435	440	445
Thr Leu Ala His Thr Tyr Asp Trp Ala Leu Ala Asp Gly Leu Met Pro		
450	455	460
Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys		
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 Met Gln His Gln Tyr Tyr Ser Leu  
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att acg atg gat gat att agc ata acc agc tta ttg gtg cca tgt act 162  
 Ile Thr Met Asp Asp Ile Ser Ile Thr Ser Leu Leu Val Pro Cys Thr  
 10 15 20

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 Phe Ile Leu Gly Phe Leu Leu Tyr Ser Phe Leu Asn Lys Lys Val  
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aag cca ctg cca cct gga ccg aag cca tgg ccc atc gtc gga aat ctg 258  
 Lys Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Val Gly Asn Leu  
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cca cat ctt ggg ccg aag ccc cac cag tcg atg gcg gcg ctg gca cg 306  
 Pro His Leu Gly Pro Lys Pro His Gln Ser Met Ala Ala Leu Ala Arg  
 60 65 70

gtg cac ggc cca tta att cat ctg aag atg ggc ttt gtg cat gtg gtt 354  
 Val His Gly Pro Leu Ile His Leu Lys Met Gly Phe Val His Val Val  
 75 80 85

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 Val Ala Ser Ser Ala Ser Val Ala Glu Lys Phe Leu Lys Val His Asp  
 90 95 100

gca aac ttc tcg agc agg cct ccc aat tcg ggt gca aaa cac gtg gcc 450  
 Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala  
 105 110 115 120

tac aac tat cag gac ttg gtc ttt gct cct tat ggc cca cgc tgg cgg Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg	125	130	135	498	
atg ctc agg aaa atc tgt gca ctc cac ctc ttc tcc gcc aaa gcc ttg Met Leu Arg Lys Ile Cys Ala Leu His Leu Phe Ser Ala Lys Ala Leu	140	145	150	546	
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gtt cta gca gat gca gga gaa acg ccg ttg aaa tta ggg cag atg atg Val Leu Ala Asp Ala Gly Glu Thr Pro Leu Lys Leu Gly Gln Met Met	170	175	180	642	
aac aca tgc gcc acc aat gca ata gcg cgt gtt atg ttg ggt cga cgc Asn Thr Cys Ala Thr Asn Ala Ile Ala Arg Val Met Leu Gly Arg Arg	185	190	195	200	690
gtg gtt gga cac gca gac tca aag gcg gag gag ttt aag gca atg gta Val Val Gly His Ala Asp Ser Lys Ala Glu Glu Phe Lys Ala Met Val	205	210	215	738	
gtg gag ttg atg gta tta gct ggt gtg ttc aac tta ggt gat ttt atc Val Glu Leu Met Val Leu Ala Gly Val Phe Asn Leu Gly Asp Phe Ile	220	225	230	786	
cca cct ctt gaa aaa ttg gat ctt caa ggt gtc att gct aag atg aag Pro Pro Leu Glu Lys Leu Asp Leu Gln Gly Val Ile Ala Lys Met Lys	235	240	245	834	
aag ctt cac ttg cgt ttc gac tcg ttc ttg agt aag atc ctt gga gac Lys Leu His Leu Arg Phe Asp Ser Phe Leu Ser Lys Ile Leu Gly Asp	250	255	260	882	
cac aag atc aac agc tca gat gaa acc aaa ggc cat tcg gat ttg ttg His Lys Ile Asn Ser Ser Asp Glu Thr Lys Gly His Ser Asp Leu Leu	265	270	275	280	930
aac atg tta att tct ttg aag gac gct gat gat gcc gaa gga ggg agg Asn Met Leu Ile Ser Leu Lys Asp Ala Asp Asp Ala Glu Gly Gly Arg	285	290	295	978	
ctc acc gac gta gaa att aaa gcg ttg ctc ttg aac ttg ttt gct gca Leu Thr Asp Val Glu Ile Lys Ala Leu Leu Asn Leu Phe Ala Ala	300	305	310	1026	
gga act gac aca aca tca agc act gtg gaa tgg tgc ata gct gag tta Gly Thr Asp Thr Thr Ser Ser Thr Val Glu Trp Cys Ile Ala Glu Leu	315	320	325	1074	
gta cga cat cct gaa atc ctt gcc caa gtc caa aaa gaa ctc gac tct Val Arg His Pro Glu Ile Leu Ala Gln Val Gln Lys Glu Leu Asp Ser	330	335	340	1122	
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Val Val Gly Lys Asn Arg Val Val Lys Glu Ala Asp Leu Ala Gly Leu			
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Pro Phe Leu Gln Ala Val Val Lys Glu Asn Phe Arg Leu His Pro Ser			
365	370	375	
acc ccg ctc tcc cta ccg agg atc gca cat gag agt tgt gaa gtg aat			1266
Thr Pro Leu Ser Leu Pro Arg Ile Ala His Glu Ser Cys Glu Val Asn			
380	385	390	
gga tac ttg att cca aag ggt tcg aca ctt ctt gtc aat gtt tgg gca			1314
Gly Tyr Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala			
395	400	405	
att gct cgc gat cca aat gtg tgg gat gaa cca cta gag ttc cgg cct			1362
Ile Ala Arg Asp Pro Asn Val Trp Asp Glu Pro Leu Glu Phe Arg Pro			
410	415	420	
gaa cga ttc ttg aag ggc ggg gaa aag cct aat gtc gat gtt aga ggg			1410
Glu Arg Phe Leu Lys Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly			
425	430	435	440
aat gat ttc gaa ttg ata ccg ttc gga gcg ggc cga aga att tgt gca			1458
Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala			
445	450	455	
gga atg agc tta gga ata cgt atg gtc cag ttg ttg aca gca act ttg			1506
Gly Met Ser Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Thr Leu			
460	465	470	
aac cat gcg ttt gac ttt gat ttg gcg gat gga cag ttg cct gaa agc			1554
Asn His Ala Phe Asp Phe Asp Leu Ala Asp Gly Gln Leu Pro Glu Ser			
475	480	485	
tta aac atg gag gaa gct tat ggg ctg acc ttg caa cga gct gac cct			1602
Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro			
490	495	500	
ttg gta gtg cac ccg aag cct agg tag gcacccatg tttatcaaac			1649
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Tyr Ser Phe Leu Asn Lys Lys Val Lys Pro Leu Pro Pro Gly Pro Lys			
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Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly Pro Lys Pro His			
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Gln Ser Met Ala Ala Leu Ala Arg Val His Gly Pro Leu Ile His Leu			
65	70	75	80
Lys Met Gly Phe Val His Val Val Ala Ser Ser Ala Ser Val Ala			
85	90	95	
Glu Lys Phe Leu Lys Val His Asp Ala Asn Phe Ser Ser Arg Pro Pro			
100	105	110	
Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe			
115	120	125	
Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile Cys Ala Leu			
130	135	140	
His Leu Phe Ser Ala Lys Ala Leu Asn Asp Phe Thr His Val Arg Gln			
145	150	155	160
Asp Glu Val Gly Ile Leu Thr Arg Val Leu Ala Asp Ala Gly Glu Thr			
165	170	175	
Pro Leu Lys Leu Gly Gln Met Met Asn Thr Cys Ala Thr Asn Ala Ile			
180	185	190	
Ala Arg Val Met Leu Gly Arg Arg Val Val Gly His Ala Asp Ser Lys			
195	200	205	
Ala Glu Glu Phe Lys Ala Met Val Val Glu Leu Met Val Leu Ala Gly			
210	215	220	
Val Phe Asn Leu Gly Asp Phe Ile Pro Pro Leu Glu Lys Leu Asp Leu			
225	230	235	240
Gln Gly Val Ile Ala Lys Met Lys Lys Leu His Leu Arg Phe Asp Ser			
245	250	255	
Phe Leu Ser Lys Ile Leu Gly Asp His Lys Ile Asn Ser Ser Asp Glu			
260	265	270	
Thr Lys Gly His Ser Asp Leu Leu Asn Met Leu Ile Ser Leu Lys Asp			
275	280	285	
Ala Asp Asp Ala Glu Gly Gly Arg Leu Thr Asp Val Glu Ile Lys Ala			
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Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Ser Thr			
305	310	315	320
Val Glu Trp Cys Ile Ala Glu Leu Val Arg His Pro Glu Ile Leu Ala			
325	330	335	
Gln Val Gln Lys Glu Leu Asp Ser Val Val Gly Lys Asn Arg Val Val			
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Lys Glu Ala Asp Leu Ala Gly Leu Pro Phe Leu Gln Ala Val Val Lys			
355	360	365	
Glu Asn Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Ile			
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Ala His Glu Ser Cys Glu Val Asn Gly Tyr Leu Ile Pro Lys Gly Ser			
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Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp			
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Asp Glu Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Lys Gly Gly Glu			
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Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Leu Ile Pro Phe			
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Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly Ile Arg Met			
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Val Gln Leu Leu Thr Ala Thr Leu Asn His Ala Phe Asp Phe Asp Leu			
465	470	475	480
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165

170

175

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ctt cac gcc aac gtt gct cac aag cat ttg att ggg aac ttc agc tgg 624  
 Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp  
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 Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly  
 210 215 220

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 Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg  
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 245 250 255

gct tct tgg aca agg tat atg gct tgc acg aaa cta acg ttt taa 813  
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Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala  
 35 40 45

Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu  
 50 55 60

Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp  
 65 70 75 80

Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg  
 85 90 95

Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser  
 100 105 110

Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp  
 115 120 125

Gly His Met Gly Leu Gly Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu  
 130 135 140

Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Ser Gly Val  
 145 150 155 160  
 Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg  
 165 170 175  
 Pro Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Asp Leu Ser Cys  
 180 185 190  
 Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp  
 195 200 205  
 Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly  
 210 215 220  
 Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg  
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 aaatggaaaa gaaacgtaca ttataaaattt atctgcaatt tgttttctct tgctaaacta 180  
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Met Ala Thr Leu Phe Leu	
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Thr Ile Leu Leu Ala Thr Val Leu Phe Leu Ile Leu Arg Ile Phe Ser	
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His Arg Arg Asn Arg Ser His Asn Asn Arg Leu Pro Pro Gly Pro Asn	
25 30 35	
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Pro Trp Pro Ile Ile Gly Asn Leu Pro His Met Gly Thr Lys Pro His	
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cga acc ctt tcc gcc atg gtt act act tac ggc cct atc ctc cac ctc	1687
Arg Thr Leu Ser Ala Met Val Thr Thr Tyr Gly Pro Ile Leu His Leu	
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Arg Leu Gly Phe Val Asp Val Val Ala Ala Ser Lys Ser Val Ala	
75 80 85	
gag cag ttc ttg aaa ata cac gac gcc aat ttc gct agc cga cca cca	1783
Glu Gln Phe Leu Lys Ile His Asp Ala Asn Phe Ala Ser Arg Pro Pro	
90 95 100	

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gcc gga gta ttt aac atc gga gat ttc gtg ccg tca ctt gat tgg tta Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu 65 70 75	2887
gat tta caa ggc gtc gct ggt aaa atg aaa cgg ctt cac aaa aga ttc	2935

Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe				
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gac gct ttt cta tcg tcg att ttg aaa gag cac gaa atg aac ggt caa				2983
Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln				
100	105	110		
gat caa aag cat aca gat atg ctt agc act tta atc tcc ctt aaa gga				3031
Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly				
115	120	125		
act gat ctt gac ggt gac gga gga agc tta acg gat act gag att aaa				3079
Thr Asp Leu Asp Gly Asp Gly Ser Leu Thr Asp Thr Glu Ile Lys				
130	135	140		
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Ala Leu Leu Leu				
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Asn Met Phe Thr Ala				
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Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu				
10	15	20		
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Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile				
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Pro Tyr Leu Gln				
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Ala Val Ile Lys Glu				
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Asn Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala				
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Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp Pro Asp Gln Trp Ser				
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agaacttga	aggat	accat	ttt	ttttt	ttg	gacaa	5597
acactttaat	gttgg	attaa	cta	acttatt	atgc	cctac	5657
gacacaagct	tgatt	gggtt	ataaaaaa	ag	tgc	actataa	5717
ttttctatga	ttttt	act	aaactt	taa	acat	ctac	5777
ttggggattt	tata	agttt	ttt	ttt	ttt	tttgcgt	5837
aacgg	ttt	caca	tta	atgt	ata	tttgcgt	5897
tttcaaa	aaagc	taat	ttt	ct	gt	tttgcgt	5957
atttcaaa	ac	aaac	ttt	tttgc	tttgc	tttgcgt	6017
tttgctttaa	aat	atgt	taa	act	tttgc	tttgcgt	6077
aagataaa	acg	caag	caatac	aatt	aggc	cct	6137
atagtgg	ttc	tagt	gga	act	gttgc	tttgcgt	6197
gaagcaac	ag	cat	cacc	aca	tttgc	tttgcgt	6257
ccggattt	aggagg	caat	atc	act	gttgc	tttgcgt	6317
caaccg	aaa	ag	cgt	ggattt	gc	cttctgtt	6377
gttctc	cg	at	gt	gt	gt	tttgcgt	6437
aaaaaaat	at	gttatttata	tttgcgtt	tttgcgt	tttgcgt	tttgcgt	6497
ttcttttta	tttcc	gggtt	tta	aaaaa	ac	aatttcaat	6557
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 <212> PRT  
 <213> *Arabidopsis thaliana*

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Met Ala Thr Leu Phe Leu Thr Ile Leu Leu Ala Thr Val Leu Phe Leu  
1 5 10 15

Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg  
20 25 30

Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His  
35 40 45

Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr  
50 55 60

Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala  
65 70 75 80

Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn  
85 90 95

Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn  
100 105 110

Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu  
115 120 125

Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp  
130 135 140

Phe Lys His Val Arg Gln  
145 150

<210> 11

<211> 147

<212> PRT

<213> *Arabidopsis thaliana*

<400> 11

Glu Glu Val Gly Thr Leu Thr Arg Glu Leu Val Arg Val Gly Thr Lys  
1 5 10 15

Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala Leu  
20 25 30

Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp His  
35 40 45

Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu Ala  
50 55 60

Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu Asp  
65 70 75 80

Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe Asp  
85 90 95

Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln Asp

100

105

110

Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly Thr  
115 120 125

Asp Leu Asp Gly Asp Gly Gly Ser Leu Thr Asp Thr Glu Ile Lys Ala  
130 135 140

Leu Leu Leu  
145

<210> 12

<211> 57

<212> PRT

<213> Arabidopsis thaliana

<400> 12

Asn Met Phe Thr Ala Gly Thr Asp Thr Ser Ala Ser Thr Val Asp Trp  
1 5 10 15

Ala Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln  
20 25 30

Glu Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser  
35 40 45

Asp Ile Ala Gln Leu Pro Tyr Leu Gln  
50 55

<210> 13

<211> 159

<212> PRT

<213> Arabidopsis thaliana

<400> 13

Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro Leu Ser  
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Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr His Ile  
20 25 30

Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp  
35 40 45

Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu  
50 55 60

Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu  
65 70 75 80

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu  
85 90 95

Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe  
100 105 110

Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn Met Glu  
115 120 125

Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val Val His  
130 135 140

Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly  
145 150 155

<210> 14

<211> 1748

<212> DNA

<213> Rosa hybrida

<220>

<221> CDS

<222> (22)...(1563)

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Met Phe Leu Ile Val Val Ile Thr Phe Leu  
1 5 10

ttc gcc gtg ttt ttg ttc cgg ctt ctt ttc tcc ggc aaa tcc caa cgc 99  
Phe Ala Val Phe Leu Phe Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg  
15 20 25

cac tcg ctc cct ctc cct ggc ccc aaa cca tgg ccg gtg gtt ggc 147  
His Ser Leu Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Val Val Gly  
30 35 40

aac tta cct cac ttg ggc ccc ttc ccg cac cac tcc atc gcg gag ttg 195  
Asn Leu Pro His Leu Gly Pro Phe Pro His His Ser Ile Ala Glu Leu  
45 50 55

gcg aag aaa cac ggg ccg ctc atg cac ctc cgc ctc ggc tac gtt gac 243  
Ala Lys Lys His Gly Pro Leu Met His Leu Arg Leu Gly Tyr Val Asp  
60 65 70

gtà gtc gtg gcg gca tca gca tcc gta gcg gcc cag ttc ttg aag act 291

Val Val Val Ala Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr  
75 80 85 90

cac gac gcc aat ttc tcc agc cga ccg ccc aac tcc ggc gcc aag cac 339  
His Asp Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His  
95 100 105

ctc gcc tat aac tac cag gac ctc gtg ttc agg ccg tac ggt cca ccg 387  
Leu Ala Tyr Asn Tyr Gln Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg  
110 115 120

tgg cgc atg ttc cgg aag atc agc tcc gtc cat ctg ttc tcc ggc aaa 435  
Trp Arg Met Phe Arg Lys Ile Ser Ser Val His Leu Phe Ser Gly Lys  
125 130 135

gcc ttg gat gat ctt aaa cac gtc cgg cag gag gag gta agt gtg cta Ala Leu Asp Asp Leu Lys His Val Arg Gln Glu Val Ser Val Leu 140 145 150	483
gcg cat gcc ttg gca aat tca ggg tca aag gta gtg aac ctg gcg caa Ala His Ala Leu Ala Asn Ser Gly Ser Lys Val Val Asn Leu Ala Gln 155 160 165 170	531
ctg ctg aac ctg tgc acg gtc aat gct cta gga agg gtg atg gta ggg Leu Leu Asn Leu Cys Thr Val Asn Ala Leu Gly Arg Val Met Val Gly 175 180 185	579
cgg agg gtt ttc ggc gac ggc agc gga ggc gac gat ccg aag gcg gac Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp 190 195 200	627
gag ttc aaa tcg atg gtg gtg gag atg atg gtg ttg gca gga gtg ttc Glu Phe Lys Ser Met Val Val Glu Met Met Val Leu Ala Gly Val Phe 205 210 215	675
aac ata ggt gac ttc atc ccc tct ctc gaa tgg ctt gac ttg caa ggc Asn Ile Gly Asp Phe Ile Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly 220 225 230	723
gtg gcg tcc aag atg aag aag ctc cac aag aga ttc gac gac ttc ttg Val Ala Ser Lys Met Lys Lys Leu His Lys Arg Phe Asp Asp Phe Leu 235 240 245 250	771
aca gcc att gtc gag gac cac aag aag ggc tcc ggc acg gcg ggg cac Thr Ala Ile Val Glu Asp His Lys Lys Gly Ser Gly Thr Ala Gly His 255 260 265	819
gtc gac atg ttg acc act ctg ctc tcc aag gaa gac gcc gac ggc Val Asp Met Leu Thr Thr Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly 270 275 280	867
gaa gga ggc aag ctc acc gat act gaa atc aaa gct ttg ctt ttg aac Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn 285 290 295	915
atg ttc acg gct ggc act gat acg tca tcg agc acg gtg gaa tgg gca Met Phe Thr Ala Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala 300 305 310	963
ata gct gaa ctc att cgg cac cct cat atg cta gcg cga gtt cag aaa Ile Ala Glu Leu Ile Arg His Pro His Met Leu Ala Arg Val Gln Lys 315 320 325 330	1011
gag ctt gac gat ttt gtt ggc cat gac cga ctt gtg acc gaa tcc gac Glu Leu Asp Asp Phe Val Gly His Asp Arg Leu Val Thr Glu Ser Asp 335 340 345	1059
ata ccc aac ctc cct tac ctc caa gcc gtg atc aag gaa acg ttc cga Ile Pro Asn Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Phe Arg 350 355 360	1107
ctc cac cca tcc act cct ctc tcc cgt atg gca gcc gag agt Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ala Glu Ser 365 370 375	1155

tgc gaa atc aac ggg tac cac atc ccg aaa ggc tcc aca ctc ttg gtc Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Leu Val 380 385 390	1203
aat gta tgg gcc ata tcg cgt gac ccg gct gaa tgg gcc gac cca ctg Asn Val Trp Ala Ile Ser Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu 395 400 405 410	1251
gag ttc aag ccc gag agg ttc ctg ccg ggg ggc gaa aag cct aat gtt Glu Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val 415 420 425	1299
gat att aga gga aac gat ttt gaa gtc ata ccc ttc ggt gcc ggg cga Asp Ile Arg Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg 430 435 440	1347
aga ata tgt gcc ggg atg agc ttg ggc ctg cgt atg gtc cat tta atg Arg Ile Cys Ala Gly Met Ser Leu Gly Leu Arg Met Val His Leu Met 445 450 455	1395
act gca aca ttg gtc cac gca ttt aat tgg gcc ttg gct gat ggg ctg Thr Ala Thr Leu Val His Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu 460 465 470	1443
acc gct gag aag tta aac atg gat gaa gca tat ggg ctc act cta caa Thr Ala Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln 475 480 485 490	1491
cga gct gca ccg tta atg gtg cac ccg cgc acc agg ctg gcc cca cag Arg Ala Ala Pro Leu Met Val His Pro Arg Thr Arg Leu Ala Pro Gln 495 500 505	1539
gca tat aaa act tca tca tct taa tttagagagct atgttctggg tggcccggt Ala Tyr Lys Thr Ser Ser Ser 510	1593
ttgatgtctc catgtttct attaggttt aaatctgtaa gataaggtga ttctatgctg 1653 aatcacaaaa gttgctatct aaattccatg tccaatgaaa acgttcttct tcccttctta 1713 taatttatga atacttatga tataggcgac agcaa	1748

<210> 15  
<211> 513  
<212> PRT  
<213> Rosa hybrida

<400> 15

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Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg His Ser Leu Pro Leu Pro 20 25 30
Pro Gly Pro Lys Pro Trp Pro Val Val Gly Asn Leu Pro His Leu Gly 35 40 45
Pro Phe Pro His His Ser Ile Ala Glu Leu Ala Lys Lys His Gly Pro 50 55 60
Leu Met His Leu Arg Leu Gly Tyr Val Asp Val Val Ala Ala Ser

65	70	75	80
Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser			
85	90	95	
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Leu Ala Tyr Asn Tyr Gln			
100	105	110	
Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg Trp Arg Met Phe Arg Lys			
115	120	125	
Ile Ser Ser Val His Leu Phe Ser Gly Lys Ala Leu Asp Asp Leu Lys			
130	135	140	
His Val Arg Gln Glu Glu Val Ser Val Leu Ala His Ala Leu Ala Asn			
145	150	155	160
Ser Gly Ser Lys Val Val Asn Leu Ala Gln Leu Leu Asn Leu Cys Thr			
165	170	175	
Val Asn Ala Leu Gly Arg Val Met Val Gly Arg Arg Val Phe Gly Asp			
180	185	190	
Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp Glu Phe Lys Ser Met Val			
195	200	205	
Val Glu Met Met Val Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Ile			
210	215	220	
Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly Val Ala Ser Lys Met Lys			
225	230	235	240
Lys Leu His Lys Arg Phe Asp Asp Phe Leu Thr Ala Ile Val Glu Asp			
245	250	255	
His Lys Lys Gly Ser Gly Thr Ala Gly His Val Asp Met Leu Thr Thr			
260	265	270	
Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly Glu Gly Lys Leu Thr			
275	280	285	
Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr			
290	295	300	
Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg			
305	310	315	320
His Pro His Met Leu Ala Arg Val Gln Lys Glu Leu Asp Asp Phe Val			
325	330	335	
Gly His Asp Arg Leu Val Thr Glu Ser Asp Ile Pro Asn Leu Pro Tyr			
340	345	350	
Leu Gln Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro			
355	360	365	
Leu Ser Leu Pro Arg Met Ala Ala Glu Ser Cys Glu Ile Asn Gly Tyr			
370	375	380	
His Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ser			
385	390	395	400
Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu Glu Phe Lys Pro Glu Arg			
405	410	415	
Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Ile Arg Gly Asn Asp			
420	425	430	
Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met			
435	440	445	
Ser Leu Gly Leu Arg Met Val His Leu Met Thr Ala Thr Leu Val His			
450	455	460	
Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu Thr Ala Glu Lys Leu Asn			
465	470	475	480
Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met			
485	490	495	
Val His Pro Arg Thr Arg Leu Ala Pro Gln Ala Tyr Lys Thr Ser Ser			
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Ser			

<211> 1660  
<212> DNA  
<213> Chrysanthemum

<220>  
<221> CDS  
<222> (4)..(1530)

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1 5 10 15

gta ctc tat gta ttt ctt aac tta agt tca cgt aaa tcc gcc aga ctc 96  
Val Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu  
20 25 30

cca ccc ggg cca aca cca tgg cct ata gtc ggg aac tta cca cac ctt 144  
Pro Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu  
35 40 45

ggc cca atc cca cac cac gca ctc gcg gcc tta gcc aag aag tac ggg 192  
Gly Pro Ile Pro His His Ala Leu Ala Leu Ala Lys Lys Tyr Gly  
50 55 60

cca ttg atg cac ctg cgg ctc ggg tgt gtg gac gtg gtt gtg gcc gcg 240  
Pro Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala  
65 70 75

tct gct tcc gta gct gca cag ttt tta aaa gtt cac gac gca aat ttt 288  
Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe  
80 85 90 95

gct agt agg ccg cca aat tct ggc gcg aaa cat gtg gcg tat aat tat 336  
Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr  
100 105 110

cag gat ctt gtg ttt gca cct tat ggt cca agg tgg cgt ttg tta agg 384  
Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg  
115 120 125

aag att tgt tcg gtc cat ttg ttt tct gct aaa gca ctt gat gat ttt 432  
Lys Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe  
130 135 140

cgt cat gtt cga cag gag gag gta gca gtc cta acc cgc gta cta ctg 480  
Arg His Val Arg Gln Glu Val Ala Val Leu Thr Arg Val Leu Leu  
145 150 155

agt gct gga aac tca ccg gta cag ctt ggc caa cta ctt aac gtg tgt 528  
Ser Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys  
160 165 170 175

gcc aca aac gcc tta gca cgg gta atg tta ggt agg aga gtt ttc gga 576  
Ala Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly  
180 185 190

gac gga att gac agg tca gcc aat gag ttc aaa gat atg gta gta gag 624  
Asp Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu  
195 200 205

tta atg gta tta gca gga gaa ttt aac ctt ggt gac ttt att cct gta Leu Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val	672
210 215 220	
ctt gac cta ttc gac cta caa ggc att act aaa aaa atg aag aag ctt Leu Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu	720
225 230 235	
cat gtt cgg ttc gat tca ttt ctt agt aag atc gtt gag gag cat aaa His Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys	768
240 245 250 255	
acg gca cct ggt ggg ttg ggt cat act gat ttg ctg agc acg ttg att Thr Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile	816
260 265 270	
tca ctt aaa gat gat gct gat att gaa ggt ggg aag ctt aca gat act Ser Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr	864
275 280 285	
gaa atc aaa gct ttg ctt ctg aat tta ttc gct gcg gga aca gac aca Glu Ile Lys Ala Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr	912
290 295 300	
tcc tct agt aca gta gaa tgg gca ata gcc gaa ctc att cgt cat cca Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro	960
305 310 315	
caa ata tta aaa caa gcc cga gaa gag ata gac gct gta gtt ggt caa Gln Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln	1008
320 325 330 335	
gac cgg ctt gta aca gaa ttg gac ttg agc caa cta aca tac ctc cag Asp Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln	1056
340 345 350	
gct ctt gtg aaa gag gtg ttt agg ctc cac cct tca acg cca ctc tcc Ala Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser	1104
355 360 365	
tta cca aga ata tca tcc gag agt tgt gag gtc gat ggg tat tat atc Leu Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile	1152
370 375 380	
cct aag gga tcc aca ctc ctc gtt aac gtg tgg gcc att gcg cga gac Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp	1200
385 390 395	
cca aaa atg tgg gcg gat cct ctt gaa ttt agg cct tct cgg ttt tta Pro Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu	1248
400 405 410 415	
ccc ggg gga gaa aag ccc ggt gct gat gtt agg gga aat gat ttt gaa Pro Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu	1296
420 425 430	
gtt ata cca ttt ggg gca gga cga agg att tgt gcg ggt atg agc cta Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu	1344
435 440 445	

ggc ttg aga atg gtc cag ttg ctc att gca aca ttg gtc caa act ttt		1392	
Gly Leu Arg Met Val Gln Leu Leu Ile Ala Thr Leu Val Gln Thr Phe			
450	455	460	
gat tgg gaa ctg gct aac ggg tta gag ccg gag atg ctc aac atg gaa		1440	
Asp Trp Glu Leu Ala Asn Gly Leu Glu Pro Glu Met Leu Asn Met Glu			
465	470	475	
gaa gcg tat gga ttg acc ctt caa cgg gct gca ccc ttg atg gtt cac		1488	
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His			
480	485	490	
ccg aag ccg agg tta gct ccc cac gta tat gaa agt att taa		1530	
Pro Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile			
500	505		
ggactagttt ctctttgcc ttttgttc gcaaaggta atgaataaac gatttcatga	1590		
ctcagatagt tatgtaaaca attgtgttg ctgttatat atttatctat tttctagaa	1650		
caaaaaaaaaa		1660	
<210> 17			
<211> 508			
<212> PRT			
<213> Chrysanthemum			
<400> 17			
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Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu Pro			
20	25	30	
Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly			
35	40	45	
Pro Ile Pro His His Ala Leu Ala Leu Ala Lys Lys Tyr Gly Pro			
50	55	60	
Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Ala Ala Ser			
65	70	75	80
Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe Ala			
85	90	95	
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln			
100	105	110	
Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys			
115	120	125	
Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Arg			
130	135	140	
His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu Ser			
145	150	155	160
Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys Ala			
165	170	175	
Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly Asp			
180	185	190	
Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu Leu			
195	200	205	
Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val Leu			
210	215	220	
Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu His			
225	230	235	240

Val	Arg	Phe	Asp	Ser	Phe	Leu	Ser	Lys	Ile	Val	Glu	Glu	His	Lys	Thr
									245		250				255
Ala	Pro	Gly	Gly	Leu	Gly	His	Thr	Asp	Leu	Leu	Ser	Thr	Leu	Ile	Ser
									260		265				270
Leu	Lys	Asp	Asp	Ala	Asp	Ile	Glu	Gly	Gly	Lys	Leu	Thr	Asp	Thr	Glu
									275		280				285
Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ala	Ala	Gly	Thr	Asp	Thr	Ser
									290		295				300
Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg	His	Pro	Gln
									305		310				320
Ile	Leu	Lys	Gln	Ala	Arg	Glu	Glu	Ile	Asp	Ala	Val	Val	Gly	Gln	Asp
									325		330				335
Arg	Leu	Val	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Leu	Thr	Tyr	Leu	Gln	Ala
									340		345				350
Leu	Val	Lys	Glu	Val	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser	Leu
									355		360				365
Pro	Arg	Ile	Ser	Ser	Glu	Ser	Cys	Glu	Val	Asp	Gly	Tyr	Tyr	Ile	Pro
									370		375				380
Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro
									385		390				400
Lys	Met	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Ser	Arg	Phe	Leu	Pro
									405		410				415
Gly	Gly	Glu	Lys	Pro	Gly	Ala	Asp	Val	Arg	Gly	Asn	Asp	Phe	Glu	Val
									420		425				430
Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Ser	Leu	Gly
									435		440				445
Leu	Arg	Met	Val	Gln	Leu	Leu	Ile	Ala	Thr	Leu	Val	Gln	Thr	Phe	Asp
									450		455				460
Trp	Glu	Leu	Ala	Asn	Gly	Leu	Glu	Pro	Glu	Met	Leu	Asn	Met	Glu	Glu
									465		470				480
Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ala	Pro	Leu	Met	Val	His	Pro
									485		490				495
Lys	Pro	Arg	Leu	Ala	Pro	His	Val	Tyr	Glu	Ser	Ile				
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<210> 18  
<211> 1815  
<212> DNA  
<213> Torenia

<220>  
<221> CDS  
<222> (107)..(1633)

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catacatcat caccgaatac gcacgctact accactgcga ttagcc atg agt ccc 115
                                         Met Ser Pro
                                         1

tta gcc ttg atg atc ata agt acc tta tta ggg ttt ctc cta tac cac 163
Leu Ala Leu Met Ile Ile Ser Thr Leu Leu Gly Phe Leu Leu Tyr His
      5           10           15

tct ctt cgc tta cta ctc ttc tcc ggc caa ggt cgc cga cta cta cca 211

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Ser	Leu	Arg	Leu	Leu	Phe	Ser	Gly	Gln	Gly	Arg	Arg	Leu	Leu	Pro		
20				25				30				35				
cca	ggc	cca	cgc	ccg	tgg	ccg	ctg	gtg	gga	aat	ctc	ccg	cac	tta	ggc	259
Pro	Gly	Pro	Arg	Pro	Trp	Pro	Leu	Val	Gly	Asn	Leu	Pro	His	Leu	Gly	
					40			45					50			
ccg	aag	cca	cac	gcc	tcc	atg	gcc	gag	ctc	gct	cga	gcc	tac	gga	ccc	307
Pro	Lys	Pro	His	Ala	Ser	Met	Ala	Glu	Leu	Ala	Arg	Ala	Tyr	Gly	Pro	
					55			60			65					
ctc	atg	cac	cta	aag	atg	ggg	ttc	gtc	cac	gtc	gtg	gtg	gct	tcg	tcg	355
Leu	Met	His	Leu	Lys	Met	Gly	Phe	Val	His	Val	Val	Val	Ala	Ser	Ser	
					70		75			80						
gct	agc	gct	gag	cag	tgc	ctg	agg	gtt	cac	gac	gct	aat	ttc	ttg		403
Ala	Ser	Ala	Ala	Glu	Gln	Cys	Leu	Arg	Val	His	Asp	Ala	Asn	Phe	Leu	
					85		90			95						
agc	agg	cca	ccc	aac	tcc	ggc	gcc	aag	cac	gtc	gct	tac	aac	tac	gag	451
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Val	Ala	Tyr	Asn	Tyr	Glu	
					100		105			110		115				
gac	ttg	gtt	ttc	aga	ccg	tac	gtt	ccc	aag	tgg	agg	ctg	ttg	agg	aag	499
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Lys	Trp	Arg	Leu	Leu	Arg	Lys	
					120		125			130						
ata	tgc	gct	cag	cat	att	ttc	tcc	gtc	aag	gct	atg	gat	gac	ttc	agg	547
Ile	Cys	Ala	Gln	His	Ile	Phe	Ser	Val	Lys	Ala	Met	Asp	Asp	Phe	Arg	
					135		140			145						
cgc	gtc	aga	gag	gaa	gag	gtg	gcc	atc	ctg	agt	cgc	gct	cta	gca	ggc	595
Arg	Val	Arg	Glu	Glu	Glu	Val	Ala	Ile	Leu	Ser	Arg	Ala	Leu	Ala	Gly	
					150		155			160						
aaa	agg	gcc	gta	ccc	ata	ggc	caa	atg	ctc	aac	gtg	tgc	gcc	aca	aac	643
Lys	Arg	Ala	Val	Pro	Ile	Gly	Gln	Met	Leu	Asn	Val	Cys	Ala	Thr	Asn	
					165		170			175						
gcc	cta	tct	cgc	gtc	atg	atg	ggg	cg	cg	gt	gt	gg	cac	gc	gt	691
Ala	Leu	Ser	Arg	Val	Met	Met	Gly	Arg	Arg	Val	Val	Gly	His	Ala	Asp	
					180		185			190		195				
gga	acc	aac	gac	gcc	aag	gct	gag	gag	ttc	aaa	gcc	atg	gtc	gtc	gag	739
Gly	Thr	Asn	Asp	Ala	Lys	Ala	Glu	Glu	Phe	Lys	Ala	Met	Val	Val	Glu	
					200		205			210						
ctc	atg	gtc	ctc	tcc	ggc	gtc	ttc	aa	atc	gt	t	tc	cc	tt		787
Leu	Met	Val	Leu	Ser	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	Phe	
					215		220			225						
ctc	gag	cct	ctc	gac	ttg	cag	gga	gtg	gct	tcc	aag	atg	aag	aaa	ctc	835
Leu	Glu	Pro	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys	Lys	Leu	
					230		235			240						
cac	gct	cg	ttc	gat	qca	ttc	ttg	acc	gag	att	qta	cga	gag	cgt	tgt	883
His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Glu	Ile	Val	Arg	Glu	Arg	Cys	
					245		250			255						

cat	ggg	cag	atc	aac	aac	agt	ggt	gct	cat	cag	gat	gat	ttg	ctt	agc	931
His	Gly	Gln	Ile	Asn	Asn	Ser	Gly	Ala	His	Gln	Asp	Asp	Leu	Leu	Ser	
260				265					270				275			
acg	ttg	att	tcg	ttc	aaa	ggg	ctt	gac	gat	ggc	gat	ggt	tcc	agg	ctc	979
Thr	Leu	Ile	Ser	Phe	Lys	Gly	Leu	Asp	Asp	Gly	Asp	Gly	Ser	Arg	Leu	
				280				285				290				
act	gac	aca	gaa	atc	aag	gcg	ctg	ctc	ttg	aac	ctt	ttg	gac	acg	acg	1027
Thr	Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Leu	Asp	Thr	Thr	
				295				300				305				
tcg	agc	acg	gtg	gaa	tgg	gcc	gta	gcc	gaa	ctc	cta	cgc	cac	cct	aag	1075
Ser	Ser	Thr	Val	Glu	Trp	Ala	Val	Ala	Glu	Leu	Leu	Arg	His	Pro	Lys	
				310			315				320					
aca	tta	gcc	caa	gtc	cg	caa	gag	ctc	gac	tcg	gtc	gtg	ggt	aag	aac	1123
Thr	Leu	Ala	Gln	Val	Arg	Gln	Glu	Leu	Asp	Ser	Val	Val	Gly	Lys	Asn	
				325			330				335					
agg	ctc	gtg	tcc	gag	acc	gat	ctg	aat	cag	ctg	ccc	tat	cta	caa	gct	1171
Arg	Leu	Val	Ser	Glu	Thr	Asp	Leu	Asn	Gln	Leu	Pro	Tyr	Leu	Gln	Ala	
				340			345				350			355		
gtc	gtc	aaa	gaa	act	tcc	cgc	ctc	cat	cct	ccg	acg	ccg	ctc	tct	cta	1219
Val	Val	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Pro	Thr	Pro	Leu	Ser	Leu	
				360			365				370					
ccg	aga	ctc	g	g	aa	g	a	g	t	g	atc	g	a	t	cc	1267
Pro	Arg	Leu	Ala	Glu	Asp	Asp	Cys	Glu	Ile	Asp	Gly	Tyr	Leu	Ile	Pro	
				375			380				385					
aag	ggc	tcg	acc	ctt	ctg	gtg	aac	gtt	tgg	gcc	ata	gcc	cgc	gat	ccc	1315
Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro	
				390			395				400					
aag	gtt	tgg	gcc	gat	ccg	ttg	gag	ttt	agg	ccc	gaa	cga	ttc	ttg	acg	1363
Lys	Val	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Leu	Thr	
				405			410				415					
ggc	gga	gaa	aag	gcc	gac	gtc	gat	gtc	aag	ggg	aac	gat	ttc	gaa	gtg	1411
Gly	Gly	Glu	Lys	Ala	Asp	Val	Asp	Val	Lys	Gly	Asn	Asp	Phe	Glu	Val	
				420			425				430			435		
ata	ccg	tcc	ggg	g	cg	g	gt	cg	agg	atc	tgc	g	ct	gg	ttg	1459
Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Val	Gly	Leu	Gly	
				440			445				450					
ata	cgt	atg	gtc	caa	ctg	ttg	acg	g	cg	agt	ttg	atc	cat	gca	ttc	1507
Ile	Arg	Met	Val	Gln	Leu	Leu	Thr	Ala	Ser	Leu	Ile	His	Ala	Phe	Asp	
				455			460				465					
ctg	gac	ctt	g	c	aat	ggg	ctt	ttg	gcc	caa	aat	ctg	aac	atg	gaa	1555
Leu	Asp	Leu	Ala	Asn	Gly	Leu	Leu	Ala	Gln	Asn	Leu	Asn	Met	Glu	Glu	
				470			475				480					
gca	tat	ggg	ctt	acg	cta	caa	cg	g	ct	ttg	ttg	gtc	cac	cct		1603
Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Glu	Pro	Leu	Leu	Val	His	Pro	
				485			490				495					

agg ccg cggttg gcc act cat gtc tat taa ttaaatttagg cctaaactac 1653  
Arg Pro Arg Leu Ala Thr His Val Tyr  
500 505

gatgaatgac ccatttaacg ttaataagag ttttcaattt atgtgagttt gcatggat 1713

gtatggatg gtgcttgtaa taaattgtat ctgttaggtg tgttcattga tgataaatct 1773

agtttgtact gctgctcaaa aaaaaaaaaa aaaaaaaaaa aa 1815

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<211> 508

<212> PRT

<213> Torenia

<400> 19

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Leu Leu Pro Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro  
35 40 45

His Leu Gly Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala  
50 55 60

Tyr Gly Pro Leu Met His Leu Lys Met Gly Phe Val His Val Val Val  
65 70 75 80

Ala Ser Ser Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala  
85 90 95

Asn Phe Leu Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr  
100 105 110

Asn Tyr Glu Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu  
115 120 125

Leu Arg Lys Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp  
130 135 140

Asp Phe Arg Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ser Arg Ala  
145 150 155 160

Leu Ala Gly Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys  
165 170 175

Ala Thr Asn Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly  
180 185 190

His Ala Asp Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met  
195 200 205

Val Val Glu Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe  
210 215 220

Ile Pro Phe Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met  
225 230 235 240

Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg  
245 250 255

Glu Arg Cys His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp  
260 265 270

Leu Leu Ser Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly  
275 280 285

Ser Arg Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Leu  
290 295 300

Asp Thr Thr Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg  
305 310 315 320

His Pro Lys Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val  
325 330 335

Gly Lys Asn Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr  
 340 345 350  
 Leu Gln Ala Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro  
 355 360 365  
 Leu Ser Leu Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr  
 370 375 380  
 Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala  
 385 390 395 400  
 Arg Asp Pro Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg  
 405 410 415  
 Phe Leu Thr Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp  
 420 425 430  
 Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val  
 435 440 445  
 Gly Leu Gly Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His  
 450 455 460  
 Ala Phe Asp Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn  
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 485 490 495  
 Val His Pro Arg Pro Arg Leu Ala Thr His Val Tyr  
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<211> 1824

<212> DNA

<213> Jap. Morning Glory

<220>

<221> CDS

<222> (2)..(1555)

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 1 5 10 15

ttt ctt att ctc agg gtg aaa cag cgt tac cct cct ctc cca ccc 97  
 Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro  
 20 25 30

gga cca aaa cca tgg ccg gtg tta gga aac ctt ccc cac ctg ggc aag 145  
 Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys  
 35 40 45

aag cct cac cag tcg att gcg gcc atg gct gag agg tac ggc ccc ctc 193  
 Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu  
 50 55 60

atg cac ctc cgc cta gga ttc gtg gac gtg gtt gtg gcc gcc tcc gcc 241  
 Met His Leu Arg Leu Gly Phe Val Asp Val Val Ala Ala Ser Ala  
 65 70 75 80

gcc gtg gcc gct cag ttc ttg aaa gtt cac gac tcg aac ttc tcc aac 289  
 Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn  
 85 90 95

cgg ccg ccg aac tcc ggc gcg gaa cac att gct tat aac tat caa gac 337

Arg Pro Pro Asn Ser Gly Ala Glu His Ile Ala Tyr Asn Tyr Gln Asp	100	105	110	
ctc gtc ttc gcg ccc tac ggc ccg cgg tgg cgc atg ctt agg aag atc				385
Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile	115	120	125	
acc tcc gtg cat ctc ttc tcg gcc aag gcg ttg gat gac ttc tgc cat				433
Thr Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Cys His	130	135	140	
gtt cgc cag gaa gag gtt gca act ctg aca cgc agt cta gca agt gca				481
Val Arg Gln Glu Glu Val Ala Thr Leu Thr Arg Ser Leu Ala Ser Ala	145	150	155	
ggc aaa act cca gta aaa cta ggg cag tta cta aac gtg tgc acc acg				529
Gly Lys Thr Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr	165	170	175	
aac gcc cta gct cgt gta atg cta ggg cgg aag gtc ttt aat gac gga				577
Asn Ala Leu Ala Arg Val Met Leu Gly Arg Lys Val Phe Asn Asp Gly	180	185	190	
ggt agc aag agc gac cca aag gcg gag gag ttc aag tcg atg gtg gag				625
Gly Ser Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Ser Met Val Glu	195	200	205	
gag atg atg gtg ttg gcc gga agt ttt aac atc ggc gat ttc att ccg				673
Glu Met Met Val Leu Ala Gly Ser Phe Asn Ile Gly Asp Phe Ile Pro	210	215	220	
gtc ttg ggt tgg ttt gac gtt cag ggt atc gta ggg aag atg aag aaa				721
Val Leu Gly Trp Phe Asp Val Gln Gly Ile Val Gly Lys Met Lys Lys	225	230	235	
ctc cac gcg cgt ttt gat gcg ttc ttg aac acc att cta gag gaa cac				769
Leu His Ala Arg Phe Asp Ala Phe Leu Asn Thr Ile Leu Glu Glu His	245	250	255	
aaa tgt gtc aac aat caa cac acg acg ttg tcg aaa gat gtg gac ttc				817
Lys Cys Val Asn Asn Gln His Thr Thr Leu Ser Lys Asp Val Asp Phe	260	265	270	
ttg agc acc cta att agg ctc aaa gat aat ggg gct gat atg gat tgt				865
Leu Ser Thr Leu Ile Arg Leu Lys Asp Asn Gly Ala Asp Met Asp Cys	275	280	285	
gaa gag gga aaa ctc acc gac act gaa att aag gct ttg ctc ttg aac				913
Glu Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn	290	295	300	
ctg ttc aca gct ggg act gat aca tca tct agc act gtg gag tgg gca				961
Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala	305	310	315	
atc gca gaa cta cta cgc aac cca aaa atc tta aac caa gca caa caa				1009
Ile Ala Glu Leu Leu Arg Asn Pro Lys Ile Leu Asn Gln Ala Gln Gln	325	330	335	
gag ctt gac tta gtg gtg ggt caa aat cag cta gtc aca gaa tct gac				1057

Glu	Leu	Asp	Leu	Val	Val	Gly	Gln	Asn	Gln	Leu	Val	Thr	Glu	Ser	Asp	
340							345					350				
tta acc gat cta cct ttc ctg caa gca ata gtg aag gag acc ttc agg															1105	
Leu	Thr	Asp	Leu	Pro	Phe	Leu	Gln	Ala	Ile	Val	Lys	Glu	Thr	Phe	Arg	
355							360				365					
cta cac cca tcc acc cca ctc tct ctt cca aga atg gga gct cag ggt															1153	
Leu	His	Pro	Ser	Thr	Pro	Leu	Ser	Leu	Pro	Arg	Met	Gly	Ala	Gln	Gly	
370							375				380					
tgc gag atc aat ggc tac ttc atc ccc aaa ggc gca acg ctt ttg gtc															1201	
Cys	Glu	Ile	Asn	Gly	Tyr	Phe	Ile	Pro	Lys	Gly	Ala	Thr	Leu	Leu	Val	
385							390			395			400			
aac gtt tgg gcc ata gct cgt gat ccc aat gtg tgg aca aat cct ctt															1249	
Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro	Asn	Val	Trp	Thr	Asn	Pro	Leu	
405							410				415					
gag ttc aac cca cac cga ttc ttg cct ggt gga gaa aag ccc aac gtg															1297	
Glu	Phe	Asn	Pro	His	Arg	Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val	
420							425				430					
gat att aaa ggg aat gac ttt gaa gtg att cct ttt gga gcc ggg cgt															1345	
Asp	Ile	Lys	Gly	Asn	Asp	Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	
435							440			445						
aga ata tgc tct ggg atg agt ttg ggg ata agg atg gtt cac ctg ttg															1393	
Arg	Ile	Cys	Ser	Gly	Met	Ser	Leu	Gly	Ile	Arg	Met	Val	His	Leu	Leu	
450							455			460						
gtt gca act ttg gtg cat gct ttt gat tgg gat ttg gtg aat gga caa															1441	
Val	Ala	Thr	Leu	Val	His	Ala	Phe	Asp	Trp	Asp	Leu	Val	Asn	Gly	Gln	
465							470			475			480			
tct gta gag acg ctc aat atg gag gaa gct tat ggt ctc acc ctt caa															1489	
Ser	Val	Glu	Thr	Leu	Asn	Met	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln		
485							490			495						
cga gct gtt cct ttg atg ttg cat cca aag ccc aga tta caa cca cat															1537	
Arg	Ala	Val	Pro	Leu	Met	Leu	His	Pro	Lys	Pro	Arg	Leu	Gln	Pro	His	
500							505				510					
ctc tat act ctc aat taa attgcaattt gattttggtg attataacaat															1585	
Leu	Tyr	Thr	Leu	Asn												
515																
tataatcgag ggacatagga tccccatcta tttatattca gttataagag acttccaaca															1645	
aagggtctagc ttgcacctt aaaagttgta aaagaggtcc tacatatgta aaagccgc															1705	
aaaggaaaac tggttgtatt caattccgct aggcttgtc cgaaagacct catgaagact															1765	
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<211> 517  
<212> PRT

<213> Jap. Morning Glory

<400> 21

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 Phe Leu Ile Leu Arg Val Lys Gln Arg Tyr Pro Leu Pro Leu Pro Pro  
 20 25 30  
 Gly Pro Lys Pro Trp Pro Val Leu Gly Asn Leu Pro His Leu Gly Lys  
 35 40 45  
 Lys Pro His Gln Ser Ile Ala Ala Met Ala Glu Arg Tyr Gly Pro Leu  
 50 55 60  
 Met His Leu Arg Leu Gly Phe Val Asp Val Val Ala Ala Ser Ala  
 65 70 75 80  
 Ala Val Ala Ala Gln Phe Leu Lys Val His Asp Ser Asn Phe Ser Asn  
 85 90 95  
 Arg Pro Pro Asn Ser Gly Ala Glu His Ile Ala Tyr Asn Tyr Gln Asp  
 100 105 110  
 Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile  
 115 120 125  
 Thr Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Cys His  
 130 135 140  
 Val Arg Gln Glu Glu Val Ala Thr Leu Thr Arg Ser Leu Ala Ser Ala  
 145 150 155 160  
  
 Gly Lys Thr Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr  
 165 170 175  
 Asn Ala Leu Ala Arg Val Met Leu Gly Arg Lys Val Phe Asn Asp Gly  
 180 185 190  
 Gly Ser Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Ser Met Val Glu  
 195 200 205  
 Glu Met Met Val Leu Ala Gly Ser Phe Asn Ile Gly Asp Phe Ile Pro  
 210 215 220  
 Val Leu Gly Trp Phe Asp Val Gln Gly Ile Val Gly Lys Met Lys Lys  
 225 230 235 240  
 Leu His Ala Arg Phe Asp Ala Phe Leu Asn Thr Ile Leu Glu Glu His  
 245 250 255  
 Lys Cys Val Asn Asn Gln His Thr Thr Leu Ser Lys Asp Val Asp Phe  
 260 265 270  
 Leu Ser Thr Leu Ile Arg Leu Lys Asp Asn Gly Ala Asp Met Asp Cys  
 275 280 285  
 Glu Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn  
 290 295 300  
 Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala  
 305 310 315 320  
 Ile Ala Glu Leu Leu Arg Asn Pro Lys Ile Leu Asn Gln Ala Gln Gln  
 325 330 335  
 Glu Leu Asp Leu Val Val Gly Gln Asn Gln Leu Val Thr Glu Ser Asp  
 340 345 350  
 Leu Thr Asp Leu Pro Phe Leu Gln Ala Ile Val Lys Glu Thr Phe Arg  
 355 360 365  
 Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Gly Ala Gln Gly  
 370 375 380  
 Cys Glu Ile Asn Gly Tyr Phe Ile Pro Lys Gly Ala Thr Leu Leu Val  
 385 390 395 400  
 Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp Thr Asn Pro Leu  
 405 410 415  
 Glu Phe Asn Pro His Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val  
 420 425 430  
 Asp Ile Lys Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg  
 435 440 445

Arg Ile Cys Ser Gly Met Ser Leu Gly Ile Arg Met Val His Leu Leu  
 450 455 460  
 Val Ala Thr Leu Val His Ala Phe Asp Trp Asp Leu Val Asn Gly Gln  
 465 470 475 480  
 Ser Val Glu Thr Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln  
 485 490 495  
 Arg Ala Val Pro Leu Met Leu His Pro Lys Pro Arg Leu Gln Pro His  
 500 505 510  
 Leu Tyr Thr Leu Asn  
 515

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 <212> DNA  
 <213> Gentian

<220>  
 <221> CDS  
 <222> (1)...(1431)

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 Pro Ile Leu Gly Asn Ile Pro His Leu Gly Ser Lys Pro His Gln Thr  
 1 5 10 15  
 ctc gcg gaa atg gcg aaa acc tac ggt ccg ctc atg cac ttg aag ttc 96  
 Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe  
 20 25 30  
 ggg ctt aag gac gcg gtg gtg gcg tcg tct gcg tcg gtg gca gag cag 144  
 Gly Leu Lys Asp Ala Val Ala Ser Ser Ala Ser Val Ala Glu Gln  
 35 40 45  
 ttt ctg aag aaa cac gac gtg aat ttc tcg aac ccg ccg cca aac tcc 192  
 Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser  
 50 55 60  
 ggg gcc aaa cat ata gct tat aac tat cag gac ctg gta ttc gct ccc 240  
 Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro  
 65 70 75 80  
 tat gga ccc cgg tgg cgg ttg ctt agg aaa atc tgt tcc gtc cat ctt 288  
 Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu  
 85 90 95  
 ttc tcg tct aag gcc ttg gat gac ttt cag cat gtt cga cat gag gag 336  
 Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu  
 100 105 110  
 ata tgc atc ctt ata cga gca ata gcg agt ggc ggt cat gct ccg gtg 384  
 Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val  
 115 120 125  
 aat tta ggc aag tta tta gga gtg tgc aca acc aat gcc ctg gca aga 432  
 Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg  
 130 135 140  
 gtg atg ctt gga aga aga gta ttc gaa ggc gac ggc ggc gag aat ccg 480

Val	Met	Leu	Gly	Arg	Arg	Val	Phe	Glu	Gly	Asp	Gly	Gly	Glu	Asn	Pro		
145						150		155						160			
cat	gcc	gac	gag	ttt	aaa	tca	atg	gtg	gtg	gag	att	atg	gtg	tta	gcc	528	
His	Ala	Asp	Glu	Phe	Lys	Ser	Met	Val	Val	Glu	Ile	Met	Val	Leu	Ala		
						165		170						175			
ggt	gca	ttc	aac	ttg	ggt	gat	ttc	atc	ccg	gtt	cta	gat	tgg	ttc	gat	576	
Gly	Ala	Phe	Asn	Leu	Gly	Asp	Phe	Ile	Pro	Val	Leu	Asp	Trp	Phe	Asp		
						180		185						190			
ttg	caa	gga	att	gct	ggt	aaa	atg	aag	aaa	ctt	cat	gcc	cgt	ttc	gac	624	
Leu	Gln	Gly	Ile	Ala	Gly	Lys	Met	Lys	Lys	Leu	His	Ala	Arg	Phe	Asp		
						195		200						205			
aag	ttt	tta	aat	ggg	atc	cta	gaa	gat	cgt	aaa	tct	aac	ggc	tct	aat	672	
Lys	Phe	Leu	Asn	Gly	Ile	Leu	Glu	Asp	Arg	Lys	Ser	Asn	Gly	Ser	Asn		
						210		215						220			
gga	gct	caa	caa	tac	gtg	gac	ttg	ctc	agt	gtg	ttg	atc	tct	ttt	caa	720	
Gly	Ala	Glu	Gln	Tyr	Val	Asp	Leu	Leu	Ser	Val	Leu	Ile	Ser	Leu	Gln		
						225		230						235		240	
gat	agt	aat	atc	gac	ggt	ggt	gac	gaa	gga	acc	aaa	ctc	aca	gat	act	768	
Asp	Ser	Asn	Ile	Asp	Gly	Gly	Asp	Glu	Gly	Thr	Lys	Ser	Asp	Thr	Asp		
						245		250						255			
gaa	atc	aaa	gct	ctc	ctt	ttg	aac	ttg	ttc	ata	gcc	gga	aca	gac	act	816	
Glu	Ile	Lys	Ala	Leu	Leu	Asn	Leu	Phe	Ile	Ala	Gly	Thr	Asp	Thr			
						260		265						270			
tca	tca	agt	act	gta	gaa	tgg	gcc	atg	gca	gaa	cta	atc	cga	aac	cca	864	
Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Arg	Asn	Pro		
						275		280						285			
aag	tta	cta	gtc	caa	gcc	caa	gaa	gag	cta	gac	aga	gta	gtc	ggg	ccg	912	
Lys	Leu	Leu	Val	Gln	Ala	Gln	Glu	Glu	Leu	Asp	Arg	Val	Val	Gly	Pro		
						290		295						300			
aac	cga	ttc	gta	acc	gaa	tct	gat	ctt	cct	caa	ctg	aca	ttc	ctt	caa	960	
Asn	Arg	Phe	Val	Thr	Glu	Ser	Asp	Leu	Pro	Gln	Leu	Thr	Phe	Leu	Gln		
						305		310						315		320	
gcc	gtc	atc	aaa	gag	act	ttc	agg	ctt	cat	cca	tcc	acc	cca	ctc	tct	1008	
Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser		
						325		330						335			
ctt	cca	cga	atg	gcg	gcg	gag	gac	tgt	gag	atc	aat	ggg	tat	tat	gtc	1056	
Leu	Pro	Arg	Met	Ala	Ala	Glu	Asp	Cys	Glu	Ile	Asn	Gly	Tyr	Tyr	Val		
						340		345						350			
tca	gaa	ggt	tcg	aca	ttg	ctc	gtc	aat	gtg	tgg	gcc	ata	gct	cgt	gat	1104	
Ser	Glu	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp		
						355		360						365			
cca	aat	gct	tgg	gcc	aat	cca	cta	gat	ttc	aac	ccg	act	cgt	ttc	ttg	1152	
Pro	Asn	Ala	Trp	Ala	Asn	Pro	Leu	Asp	Phe	Asn	Pro	Thr	Arg	Phe	Leu		
						370		375						380			
gcc	ggt	gga	gag	aag	cct	aat	gtt	gat	gtt	aaa	ggg	aat	gat	ttt	gaa	1200	

Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu  
 385 390 395 400

gtg ata cct ttc ggt gct ggg cgc agg ata tgt gcc gga atg agc tta 1248  
 Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu  
 405 410 415

ggt ata cgg atg gtt caa cta gta acg gct tcg tta gtt cat tcg ttt 1296  
 Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe  
 420 425 430

gat tgg gct ttg ttg gat gga ctt aaa ccc gag aag ctt gac atg gag 1344  
 Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu  
 435 440 445

gaa ggt tat gga cta acg ctt caa cga gct tca cct tta atc gtc cat 1392  
 Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His  
 450 455 460

cca aag ccg agg ctc tcg gct caa gtt tat tgt atg taa caagtttg 1441  
 Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met  
 465 470 475

aagccagtct gatttcagtt ggatttttagt ttatttatgt atcattttgtt attttatttt 1501  
 gtatttcggt tgaatacat aaaggaaagg tggatcgctct gctgtataat agcgacgttt 1561  
 taacgtgttg tgatagtacc gtgtttact aaaacgtgtt cgtttgattt tttatagttat 1621  
 taaaaaaaaata aacagctgga ttttgaaccaaaaaaaaaaaa aaaaaaaaaa 1667

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 <212> PRT  
 <213> Gentian

<400> 23  
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 Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe  
 20 25 30  
 Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln  
 35 40 45  
 Phe Leu Lys Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser  
 50 55 60  
 Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro  
 65 70 75 80  
 Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu  
 85 90 95  
 Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu  
 100 105 110  
 Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val  
 115 120 125  
 Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg  
 130 135 140

Val Met Leu Gly Arg Arg Val Phe Glu Gly Asp Gly Gly Glu Asn Pro  
 145 150 155 160  
 His Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala

165	170	175	
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Val Leu Asp Trp Phe Asp			
180	185	190	
Leu Gln Gly Ile Ala Gly Lys Met Lys Lys Leu His Ala Arg Phe Asp			
195	200	205	
Lys Phe Leu Asn Gly Ile Leu Glu Asp Arg Lys Ser Asn Gly Ser Asn			
210	215	220	
Gly Ala Glu Gln Tyr Val Asp Leu Leu Ser Val Leu Ile Ser Leu Gln			
225	230	235	240
Asp Ser Asn Ile Asp Gly Gly Asp Glu Gly Thr Lys Leu Thr Asp Thr			
245	250	255	
Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Ile Ala Gly Thr Asp Thr			
260	265	270	
Ser Ser Ser Thr Val Glu Trp Ala Met Ala Glu Leu Ile Arg Asn Pro			
275	280	285	
Lys Leu Leu Val Gln Ala Gln Glu Glu Leu Asp Arg Val Val Gly Pro			
290	295	300	
Asn Arg Phe Val Thr Glu Ser Asp Leu Pro Gln Leu Thr Phe Leu Gln			
305	310	315	320
Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser			
325	330	335	
Leu Pro Arg Met Ala Ala Glu Asp Cys Glu Ile Asn Gly Tyr Tyr Val			
340	345	350	
Ser Glu Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp			
355	360	365	
Pro Asn Ala Trp Ala Asn Pro Leu Asp Phe Asn Pro Thr Arg Phe Leu			
370	375	380	
Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu			
385	390	395	400
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu			
405	410	415	
Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe			
420	425	430	
Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu			
435	440	445	
Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His			
450	455	460	
Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met			
465	470	475	

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 <211> 1214  
 <212> DNA  
 <213> Lisianthus

<220>  
 <221> CDS  
 <222> (2)..(1093)

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 Arg Ile Leu Thr Arg Ser Ile Ala Ser Ala Gly Glu Asn Pro Ile Asn  
 1 5 10 15

tta ggt caa tta ctc ggg gtg tgt acc aca aat gct ctg gcg aga gtg 97  
 Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val  
 20 25 30

atg ctt gga agg agg gta ttc ggc gat ggg agc ggc ggc gta gat cct Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro 35 40 45	145
cag gcg gac gag ttc aaa tcc atg gtg gtg gaa atc atg gtg ttg gcc Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala 50 55 60	193
ggc gcg ttt aat cta ggt gat ttt att ccc gct ctt gat tgg ttc gat Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp 65 70 75 80	241
ctg cag gga att acg gca aaa atg aag aaa gtt cac gct cgt ttc gat Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp 85 90 95	289
gcg ttc tta gac gcg atc ctt gag gag cac aaa tcc aac ggc tct cgc Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg 100 105 110	337
gga gct aag caa cac gtt gac ttg ctg agt atg ttg atc tcc ctt caa Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln 115 120 125	385
gat aat aac att gat ggt gaa agt ggc gcc aaa ctc act gat aca gaa Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu 130 135 140	433
atc aaa gct ttg ctt ctg aac ttg ttc acg gct gga aca gac acg tca Ile Lys Ala Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser 145 150 155 160	481
tca agt act gtg gag tgg gca atc gca gag cta atc cga aac cca gaa Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu 165 170 175	529
gta ttg gtt caa gcc caa caa gag ctc gat aga gta gtt ggg cca agt Val Leu Val Gln Ala Gln Glu Leu Asp Arg Val Val Gly Pro Ser 180 185 190	577
cgt ctt gtg acc gaa tct gat ctg cct caa ttg gca ttc ctt caa gct Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala 195 200 205	625
gtc atc aaa gag act ttc aga ctt cat cca tcc act cca ctc tct ctt Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu 210 215 220	673
cca cga atg gct tca gag ggt tgt gaa atc aat gga tac tcc atc cca Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro 225 230 235 240	721
aag ggt tcg aca ttg ctc gtt aac gta tgg tcc ata gcc cgt gat cct Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro 245 250 255	769
agt ata tgg gcc gac cca tta gaa ttt agg ccg gca cgt ttc ttg ccc Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro 260 265 270	817

ggc gga gaa aag ccc aat gtt gat gtg aga ggc aat gat ttt gag gtc	865		
Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val			
275	280	285	
ata cca ttt ggt gct gga cgt agg ata tgt gct gga atg agc ttg ggt	913		
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly			
290	295	300	
tta aga atg gtt caa ctt tcg aca gct act ttg gtt cat tcg ttt aat	961		
Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn			
305	310	315	320
tgg gat ttg ctg aat ggg atg agc cca gat aaa ctt gac atg gaa gaa	1009		
Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu			
325	330	335	
gct tat ggg ctt aca ttg caa cgg gct tca cct ttg att gtc cac cca	1057		
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro			
340	345	350	
aag ccc agg ctt gct agc tct atg tat gtt aaa tga aattatgctg	1103		
Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys			
355	360		
tgCGAATAAT tccttattta tagcaggaaa tgcatctt aattatgtgt aatgttcttc	1163		
taacttcga tggaagtgc aacaagttt tattaaaaaa aaaaaaaaaa a	1214		

<210> 25  
 <211> 363  
 <212> PRT  
 <213> Lisanthus

<400> 25  
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 20 25 30  
 Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro  
 35 40 45  
 Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala  
 50 55 60  
 Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp  
 65 70 75 80  
 Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp  
 85 90 95  
 Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg  
 100 105 110  
 Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln  
 115 120 125  
 Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu  
 130 135 140  
 Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser  
 145 150 155 160  
 Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu  
 165 170 175  
 Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser  
 180 185 190  
 Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala

195	200	205	
Val Ile Lys Glu Thr Phe Arg	Leu His Pro Ser Thr	Pro Leu Ser Leu	
210	215	220	
Pro Arg Met Ala Ser Glu Gly Cys	Glu Ile Asn Gly Tyr	Ser Ile Pro	
225	230	235	240
Lys Gly Ser Thr Leu Leu Val Asn Val	Trp Ser Ile Ala Arg	Asp Pro	
245	250	255	
Ser Ile Trp Ala Asp Pro Leu Glu	Phe Arg Pro Ala Arg	Phe Leu Pro	
260	265	270	
Gly Gly Glu Lys Pro Asn Val Asp	Val Arg Gly Asn Asp	Phe Glu Val	
275	280	285	
Ile Pro Phe Gly Ala Gly Arg Arg	Ile Cys Ala Gly Met	Ser Leu Gly	
290	295	300	
Leu Arg Met Val Gln Leu Ser Thr Ala	Thr Leu Val His Ser	Phe Asn	
305	310	315	320
Trp Asp Leu Leu Asn Gly Met Ser Pro	Asp Lys Leu Asp Met	Glu Glu	
325	330	335	
Ala Tyr Gly Leu Thr Leu Gln Arg Ala	Ser Pro Leu Ile Val	His Pro	
340	345	350	
Lys Pro Arg Leu Ala Ser Ser Met	Tyr Val Lys		
355	360		

<210> 26

<211> 1757

<212> DNA

<213> Petunia sp.

<220>

<221> CDS

<222> (35)..(1525)

<400> 26

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			Met	Asp	Tyr	Val	Asn Ile Leu
			1			5	

ctg gga ctg ttt ttc	act tgg ttc	ttg gtg	aat gga	ctc atg	tca ctt	103
Leu Gly Leu Phe Phe	Thr Trp Phe	Leu Val Asn Gly	Leu Met Ser	Leu		
10	15	20				

cga aga aga aaa atc	tct aag aaa ctt	cca cca ggt	cca ttt cct	ttg	151
Arg Arg Arg Lys Ile	Ser Lys Lys Leu	Pro Pro Gly	Pro Phe	Pro Leu	
25	30	35			

cct atc atc gga aat	ctt cac tta	ctt ggt	aat cat	cct cac	aaa tca	199
Pro Ile Ile Gly	Asn Leu His	Leu Gly	Asn His	Pro His	Lys Ser	
40	45	50		55		

ctt gct caa ctt gca	aaa att cat	ggt cct att	atg aat	ctc aaa tta	247
Leu Ala Gln Leu Ala	Lys Ile His	Gly Pro Ile	Met Asn	Leu Lys Leu	
60	65		70		

ggc caa cta aac aca	gtg gtc	att tca tca	tca gtc	gtg gca	aga gaa	295
Gly Gln Leu Asn Thr	Val Val Ile	Ser Ser Val	Val Val Ala	Arg Glu		
75	80		85			

gtc ttg caa aaa caa	gac tta aca ttt	tcc aat	agg ttt	gtc ccg	gac	343
Val Leu Gln Lys Gln	Asp Leu Thr Phe	Ser Asn Arg	Phe Val	Pro Asp		

90	95	100	
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gtc aat tct cga tgg aaa acg ctt cgc aaa atc atg aac tct agc atc Val Asn Ser Arg Trp Lys Thr Leu Arg Lys Ile Met Asn Ser Ser Ile 120	125	130	439
ttt tct ggt aac aag ctt gat ggt aat caa cat ctg agg tct aaa aag Phe Ser Gly Asn Lys Leu Asp Gly Asn Gln His Leu Arg Ser Lys Lys 140	145	150	487
gtc caa gag tta att gat tat tgt caa aag tgt gcc aag aat ggc gaa Val Gln Glu Leu Ile Asp Tyr Cys Gln Lys Cys Ala Lys Asn Gly Glu 155	160	165	535
gca gtg gat ata gga aga gca act ttt gga act act ttg aat ttg cta Ala Val Asp Ile Gly Arg Ala Thr Phe Gly Thr Thr Leu Asn Leu Leu 170	175	180	583
tcc aac acc att ttc tct aaa gat ttg act aat ccg ttt tct gat tct Ser Asn Thr Ile Phe Ser Lys Asp Leu Thr Asn Pro Phe Ser Asp Ser 185	190	195	631
gct aaa gag ttt aag gaa ttg gtt tgg aac att atg gtt gag gct gga Ala Lys Glu Phe Lys Glu Leu Val Trp Asn Ile Met Val Glu Ala Gly 200	205	210	679
aaa ccc aat ttg gtg gac tac ttt cct ttc ctt gag aaa att gat ccg Lys Pro Asn Leu Val Asp Tyr Phe Pro Phe Leu Glu Lys Ile Asp Pro 220	225	230	727
caa ggt ata aag cga cgc atg act aat aat ttt act aag ttt ctt ggc Gln Gly Ile Lys Arg Arg Met Thr Asn Asn Phe Thr Lys Phe Leu Gly 235	240	245	775
ctt atc agc ggt ttg att gat gac cgg tta aag gaa agg aat cta agg Leu Ile Ser Gly Leu Ile Asp Asp Arg Leu Lys Glu Arg Asn Leu Arg 250	255	260	823
gac aat gca aat att gat gtt tta gac gcc ctt ctc aac att agc caa Asp Asn Ala Asn Ile Asp Val Leu Asp Ala Leu Leu Asn Ile Ser Gln 265	270	275	871
gag aac cca gaa gag att gac agg aat caa atc gag cag ttg tgt ctg Glu Asn Pro Glu Glu Ile Asp Arg Asn Gln Ile Glu Gln Leu Cys Leu 280	285	290	919
gac ttg ttt gca gca ggg act gat act aca tcg aat acc ttg gag tgg Asp Leu Phe Ala Ala Gly Thr Asp Thr Ser Asn Thr Leu Glu Trp 300	305	310	967
gca atg gca gaa cta ctt cag aat cca cac aca ttg cag aaa gca caa Ala Met Ala Glu Leu Leu Gln Asn Pro His Thr Leu Gln Lys Ala Gln 315	320	325	1015
gaa gaa ctt gca caa gtc att ggt aaa ggc aaa caa gta gaa gaa gca Glu Glu Leu Ala Gln Val Ile Gly Lys Gly Lys Gln Val Glu Glu Ala			1063

330

335

340

gat gtt gga cga cta cct tac ttg cga tgc ata gtg aaa gaa acc tta			1111
Asp Val Gly Arg Leu Pro Tyr Leu Arg Cys Ile Val Lys Glu Thr Leu			
345	350	355	
cga ata cac cca gcg gct cct ctc tta att cca cgt aaa gtg gag gaa			1159
Arg Ile His Pro Ala Ala Pro Leu Leu Ile Pro Arg Lys Val Glu Glu			
360	365	370	375
gac gtt gag ttg tct acc tat att att cca aag gat tca caa gtt cta			1207
Asp Val Glu Leu Ser Thr Tyr Ile Ile Pro Lys Asp Ser Gln Val Leu			
380	385	390	
gtg aac gta tgg gca att gga cgc aac tct gat cta tgg gaa aat cct			1255
Val Asn Val Trp Ala Ile Gly Arg Asn Ser Asp Leu Trp Glu Asn Pro			
395	400	405	
ttg gtc ttt aag cca gaa agg ttt tgg gag tca gaa ata gat atc cga			1303
Leu Val Phe Lys Pro Glu Arg Phe Trp Glu Ser Glu Ile Asp Ile Arg			
410	415	420	
ggt cga gat ttt gaa ctc att cca ttt ggt gct ggt cga aga att tgc			1351
Gly Arg Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys			
425	430	435	
cct gga ttg cct ttg gct atg agg atg att cca gta gca cta ggt tca			1399
Pro Gly Leu Pro Leu Ala Met Arg Met Ile Pro Val Ala Leu Gly Ser			
440	445	450	455
ttg cta aac tca ttt aat tgg aaa cta tat ggt gga att gca cct aaa			1447
Leu Leu Asn Ser Phe Asn Trp Lys Leu Tyr Gly Gly Ile Ala Pro Lys			
460	465	470	
gat ttg gac atg cag gaa aag ttt ggc att acc ttg gcg aaa gcc caa			1495
Asp Leu Asp Met Gln Glu Lys Phe Gly Ile Thr Leu Ala Lys Ala Gln			
475	480	485	
cct ctg cta gct atc cca act ccc ctg tag ctatagggat aaattaagtt			1545
Pro Leu Leu Ala Ile Pro Thr Pro Leu			
490	495		
gaggtttaa gttactagta gattctattt cagctatagg atttctttca ccatcacgt 1605			
tgctttaccc ttggatgtg gaaagaata tctatagctt tgggtttgtt tagtttgcac 1665			
ataaaaaattt aatgaatgga ataccatgga gttataagaa ataataagac tatgattctt 1725			
accctacttg aacaatgaca tggctatttc ac 1757			

&lt;210&gt; 27

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:oligonucleotide

<400> 27  
ttttttttt tttttta

18

<210> 28  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 28  
ttttttttt ttttttc

18

<210> 29  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 29  
ttttttttt ttttttg

18

<210> 30  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 30  
Trp Ala Ile Gly Arg Asp Pro  
1 5

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified Base  
<222> (6)  
<223> n is inosine

<220>  
<221> Modified Base  
<222> (9)  
<223> n is inosine

<220>  
<221> Modified Base  
<222> (12)  
<223> n is inosine

<220>  
<221> Modified Base  
<222> (15)  
<223> n is inosine

<400> 31  
tgggcnatng gnmgnngaycc

20

<210> 32  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 32  
Phe Arg Pro Glu Arg Phe  
1 5

<210> 33  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: oligonucleotide

<220>  
<221> Modified base  
<222> (11)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (14)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (20)  
<223> n is inosine

<400> 33  
aggaaattymg nccngarmgn tt

22

<210> 34  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified base  
<222> (3)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (9)  
<223> n is inosine

<220>  
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<222> (12)  
<223> n is inosine

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<223> n is inosine

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<223> n is inosine

<220>  
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<222> (21)  
<223> n is inosine

<220>  
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<222> (24)  
<223> n is inosine

<220>  
<221> Modified base  
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<223> n is inosine

<400> 34  
ccnttyggng cnggnmgnmg natntgkscn gg

<210> 35  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<220>  
<221> UNSURE  
<222> (3)  
<223> Xaa can be any amino acid.

<400> 35  
Glu Phe Xaa Pro Glu Arg Phe  
1 5

<210> 36  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
<221> Modified base  
<222> (3)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (7)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (8)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (9)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (12)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (15)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (18)  
<223> n is inosine

<400> 36  
ganttynnc cnganmgntt

20

<210> 37  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 37  
ccacacgagt agttttggca tttgaccc

28

<210> 38  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 38  
gtcttggaca tcacac ttca atctg

25

<210> 39  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<400> 39  
ccgaattccc cccccc

17

<210> 40  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:oligonucleotide

<220>  
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<222> (3)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (9)  
<223> n is inosine

<220>  
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<222> (12)  
<223> n is inosine

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<223> n is inosine

<220>  
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<222> (24)  
<223> n is inosine

<220>  
<221> Modified base  
<222> (30)  
<223> n is inosine

<400> 40  
ccnggrcana tnckyytncc ngcncraan gg

32

<210> 41  
<211> 496  
<212> PRT  
<213> Petunia sp.

<400> 41

Met Asp Tyr Val Asn Ile Leu Leu Gly Leu Phe Phe Thr Trp Phe Leu  
1 5 10 15  
Val Asn Gly Leu Met Ser Leu Arg Arg Arg Lys Ile Ser Lys Lys Leu  
20 25 30  
Pro Pro Gly Pro Phe Pro Leu Pro Ile Ile Gly Asn Leu His Leu Leu  
35 40 45  
Gly Asn His Pro His Lys Ser Leu Ala Gln Leu Ala Lys Ile His Gly  
50 55 60  
Pro Ile Met Asn Leu Lys Leu Gly Gln Leu Asn Thr Val Val Ile Ser  
65 70 75 80  
Ser Ser Val Val Ala Arg Glu Val Leu Gln Lys Gln Asp Leu Thr Phe  
85 90 95  
Ser Asn Arg Phe Val Pro Asp Val Val His Val Arg Asn His Ser Asp  
100 105 110  
Phe Ser Val Val Trp Leu Pro Val Asn Ser Arg Trp Lys Thr Leu Arg  
115 120 125  
Lys Ile Met Asn Ser Ser Ile Phe Ser Gly Asn Lys Leu Asp Gly Asn  
130 135 140  
  
Gln His Leu Arg Ser Lys Lys Val Gln Glu Leu Ile Asp Tyr Cys Gln  
145 150 155 160  
Lys Cys Ala Lys Asn Gly Glu Ala Val Asp Ile Gly Arg Ala Thr Phe  
165 170 175  
Gly Thr Thr Leu Asn Leu Leu Ser Asn Thr Ile Phe Ser Lys Asp Leu  
180 185 190  
Thr Asn Pro Phe Ser Asp Ser Ala Lys Glu Phe Lys Glu Leu Val Trp  
195 200 205  
Asn Ile Met Val Glu Ala Gly Lys Pro Asn Leu Val Asp Tyr Phe Pro  
210 215 220  
Phe Leu Glu Lys Ile Asp Pro Gln Gly Ile Lys Arg Arg Met Thr Asn  
225 230 235 240  
Asn Phe Thr Lys Phe Leu Gly Leu Ile Ser Gly Leu Ile Asp Asp Arg  
245 250 255  
Leu Lys Glu Arg Asn Leu Arg Asp Asn Ala Asn Ile Asp Val Leu Asp  
260 265 270  
Ala Leu Leu Asn Ile Ser Gln Glu Asn Pro Glu Glu Ile Asp Arg Asn  
275 280 285  
Gln Ile Glu Gln Leu Cys Leu Asp Leu Phe Ala Ala Gly Thr Asp Thr  
290 295 300  
Thr Ser Asn Thr Leu Glu Trp Ala Met Ala Glu Leu Leu Gln Asn Pro  
305 310 315 320  
His Thr Leu Gln Lys Ala Gln Glu Glu Leu Ala Gln Val Ile Gly Lys  
325 330 335  
Gly Lys Gln Val Glu Glu Ala Asp Val Gly Arg Leu Pro Tyr Leu Arg

340	345	350	
Cys Ile Val Lys Glu Thr Leu Arg Ile His Pro Ala Ala Pro Leu Leu			
355	360	365	
Ile Pro Arg Lys Val Glu Glu Asp Val Glu Leu Ser Thr Tyr Ile Ile			
370	375	380	
Pro Lys Asp Ser Gln Val Leu Val Asn Val Trp Ala Ile Gly Arg Asn			
385	390	395	400
Ser Asp Leu Trp Glu Asn Pro Leu Val Phe Lys Pro Glu Arg Phe Trp			
405	410	415	
Glu Ser Glu Ile Asp Ile Arg Gly Arg Asp Phe Glu Leu Ile Pro Phe			
420	425	430	
Gly Ala Gly Arg Arg Ile Cys Pro Gly Leu Pro Leu Ala Met Arg Met			
435	440	445	
Ile Pro Val Ala Leu Gly Ser Leu Leu Asn Ser Phe Asn Trp Lys Leu			
450	455	460	
Tyr Gly Gly Ile Ala Pro Lys Asp Leu Asp Met Gln Glu Lys Phe Gly			
465	470	475	480
Ile Thr Leu Ala Lys Ala Gln Pro Leu Leu Ala Ile Pro Thr Pro Leu			
485	490	495	

<210> 42

<211> 513

<212> PRT

<213> *Arabidopsis thaliana*

<400> 42

Met Ala Thr Leu Phe Leu Thr Ile Leu Leu Ala Thr Val Leu Phe Leu			
1	5	10	15

Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg			
20	25	30	

Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His			
35	40	45	

Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr			
50	55	60	

Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala			
65	70	75	80

Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn			
85	90	95	

Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn			
100	105	110	

Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu			
115	120	125	

Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp			
130	135	140	

Phe Lys His Val Arg Gln Glu Glu Val Gly Thr Leu Thr Arg Glu Leu			
145	150	155	160

Val Arg Val Gly Thr Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met			
165	170	175	

Cys Val Val Asn Ala Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe

180	185	190
Gly Ala Asp Ala Asp His Lys Ala Asp Glu Phe Arg Ser Met Val Thr		
195	200	205
Glu Met Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro		
210	215	220
Ser Leu Asp Trp Leu Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg		
225	230	235
Leu His Lys Arg Phe Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His		
245	250	255
Glu Met Asn Gly Gln Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu		
260	265	270
Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly Asp Gly Ser Leu Thr		
275	280	285
Asp Thr Glu Ile Lys Ala Leu Leu Asn Met Phe Thr Ala Gly Thr		
290	295	300
Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu Ile Arg		
305	310	315
His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile Val Val		
325	330	335
Gly Arg Asp Arg Pro Val Asn Glu Ser Asp Ile Ala Gln Leu Pro Tyr		
340	345	350
Leu Gln Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro		
355	360	365
Leu Ser Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr		
370	375	380
His Ile Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala		
385	390	395
Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg		
405	410	415
Phe Leu Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp		
420	425	430
Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu		
435	440	445
Ser Leu Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln		
450	455	460
Gly Phe Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn		
465	470	475
Met Glu Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val		
485	490	495

Val His Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser  
500 505 510

Gly

<210> 43  
<211> 7  
<212> PRT  
<213> *Arabidopsis thaliana*

<400> 43  
Arg Pro Pro Asn Ser Gly Ala  
1 5

<210> 44  
<211> 17  
<212> PRT  
<213> *Arabidopsis thaliana*

<220>  
<221> UNSURE  
<222> (8)  
<223> Xaa can be any amino acid.

<220>  
<221> UNSURE  
<222> (10)  
<223> Xaa cab be any amino acid.

<220>  
<221> UNSURE  
<222> (15)  
<223> Xaa can be any amino acid.

<400> 44  
Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp  
1 5 10 15

Leu

<210> 45  
<211> 521  
<212> PRT  
<213> *Arabidopsis thaliana*

<220>  
<221> UNSURE  
<222> (8)  
<223> Xaa can be any amino acid.

<220>  
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<223> Xaa cab be any amino acid.

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<221> UNSURE

<222> (15)

<223> Xaa can be any amino acid.

<220>

<221> UNSURE

<222> (18)..(517)

<223> Xaa can be any amino acid. Positions 18-517  
can be 0-500 amino acids.

<400> 45

Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp  
1 5 10 15

Leu Xaa  
20 25 30

Xaa  
35 40 45

Xaa  
50 55 60

Xaa  
65 70 75 80

Xaa  
85 90 95

Xaa  
100 105 110

Xaa  
115 120 125

Xaa  
130 135 140

Xaa  
145 150 155 160

Xaa  
165 170 175

Xaa  
180 185 190

Xaa  
195 200 205

Xaa  
210 215 220

Xaa  
225 230 235 240

Xaa  
245 250 255

Xaa			
260	265	270	
Xaa			
275	280	285	
Xaa			
290	295	300	
Xaa			
305	310	315	320
Xaa			
325	330	335	
Xaa			
340	345	350	
Xaa			
355	360	365	
Xaa			
370	375	380	
Xaa			
385	390	395	400
Xaa			
405	410	415	
Xaa			
420	425	430	
Xaa			
435	440	445	
Xaa			
450	455	460	
Xaa			
465	470	475	480
Xaa			
485	490	495	
Xaa			
500	505	510	
Xaa Xaa Xaa Xaa Gly Gly Glu Lys			
515	520		